

SEQUENCE LISTING

<110> Pfizer Inc.
Harland, Lee

<120> Novel Polypeptide

<130> PC10970AGLK

<150> GB0101739.1
<151> 2001-01-23

<150> US 60/267,341
<151> 2001-02-08

<160> 3

<170> PatentIn version 3.1

<210> 1
<211> 918
<212> DNA
<213> Homo sapiens

<400> 1
atgcctggcc acaataacctc caggaattcc tcttgcgatc ctatagtgac accccactta 60
atcagcctct acttcatagt gcttattggc gggctggtgg gtgtcatttc cattcttttc 120
ctcctgggtga aaatgaacac ccggtcagtg accaccatgg cggtcattaa cttgggtggtg 180
gtccacagcg tttttctgct gacagtgcc a tttcgcttga cctacctcat caagaagact 240
tggtatgtttg ggctgccctt ctgcaaattt gtgagtgcc t gctgcacat ccacatgtac 300
ctcacgttcc tattctatgt ggtgatcctg gtcaccagat acctcatctt cttcaagtgc 360
aaagacaaag tggaattcta cagaaaactg catgctgtgg ctgccagtgc tggcatgtgg 420
acgctgggtga ttgtcattgt ggtacccctg gttgtctccc ggtatggaat ccatgaggaa 480
tacaatgagg agcactgttt taaatttcac aaagagcttg cttacacata tgtgaaaatc 540
atcaactata tgatagtcac ttttgtcata gccgttgctg tgattctgtt ggtcttccag 600
gtcttcatca ttatgttgat ggtgcagaag ctacgccact ctttactatc ccaccaggag 660
ttctgggctc agctgaaaaa cctatttttt ataggggtca tccttgtttg tttccttccc 720
taccagttct ttaggatcta ttacttgaat gttgtgacgc attccaatgc ctgtaacagc 780
aaggttgcat tttataacga aatcttcttg agtgtaacag caattagctg ctatgatttg 840
cttctctttg tctttggggg aagccattgg ttttaagcaa agataattgg cttatggaat 900
tgtgttttgt gccgttag 918

<210> 2
<211> 305
<212> PRT
<213> Homo sapiens

<400> 2

Met Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val
1 5 10 15

Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu
20 25 30

Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg
35 40 45

Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val
50 55 60

Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr
65 70 75 80

Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His
85 90 95

Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr
100 105 110

Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg
115 120 125

Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile
130 135 140

Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu
145 150 155 160

Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr
165 170 175

Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val
180 185 190

Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val

10055105.012302

195

200

205

Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln
 210 215 220

Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro
 225 230 235 240

Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn
 245 250 255

Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val
 260 265 270

Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser
 275 280 285

His Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys
 290 295 300

Arg
 305

<210> 3
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 3

Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp
 1 5 10 15

Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
 20 25 30

Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu
 35 40 45

Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
 50 55 60

Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val
 65 70 75 80

10055106-042306

Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
85 90 95

Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
100 105 110

Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro
115 120 125

Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
130 135 140

Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met
145 150 155 160

Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro
165 170 175

Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val
180 185 190

Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Ile Val Cys
195 200 205

Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn
210 215 220

Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala
225 230 235 240

Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His
245 250 255

Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
260 265 270

Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
275 280 285

Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
290 295 300

10055106 012302

Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
305 310 315 320

Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys
325 330 335

Val

10055106.012302